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dbEST Id: 925462  
EST name: zt19g05.r1  
GenBank Acc: AA283751  
GenBank gi: 1928032

Clone Id: IMAGE:713624 (5')  
Source: IMAGE Consortium, LLNL  
Insert length: 857  
DNA type: cDNA

Sequencing: -28m13 rev2 ET from Amersham  
PolyA Tail: Unknown

ATTCGGAACGAGGGAAAATCTGCCTTCTCACCATGAGGCTTCTAGTCCTTTCCAGCCTGC  
TCTGTATCCTGCTTCTCTGCTTCTCCATCTTCTCCACAGAAGGGAAGAGGCGTCTGCCA  
ACAGCCTGGTCAGGCAGGAGAACCAGGCTCTGCTGCCACCGAGTCCCTAGCCCCAACTCA  
ACAAACCTGAAAGGACATCATGTGAGGCTCTGTAAACCATGCAAGCTTGACCAGAGCCCG  
CTTTGGCTGTGCTGGGGATCCACAGGTGTAGCACTCCAAAGCAAGACTCCAGACAGCGG  
AGAACCTCATGCCTGGCACCTGAGGTACCCAGCAGCCTCCTGTCTCCCCTTTCAGCCTTC  
ACAGCAGTGAGCTGCAATGTTGGAGGGCTTCATCTCGGG

Quality: High quality sequence stops at base: 347

Entry Created: Apr 2 1997

Last Updated: Aug 8 1997

This clone is available royalty-free through LLNL ; contact the IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.

```

Lib Name:      Soares ovary tumor NbHOT
Organism:      Homo sapiens
Sex:           Female
Organ:          ovary
Tissue type:    ovarian tumor
Lab host:       DH10B (ampicillin resistant)
Vector:         pT7T3D (Pharmacia) with a modified polylinker
R. Site 1:      Not I
R. Site 2:      Eco RI
Description:     1st strand cDNA was primed with a Not I - oligo(dT) primer
                  [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCGGTTTTTTTTTTTTTTTTTTT 3']

```

double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo.

**SUBMITTER**

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**CITATIONS**

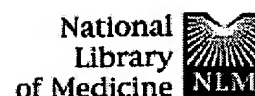
Medline UID: [97044478](#)  
Title: Generation and analysis of 280,000 human expressed sequence tags  
Authors: Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissole, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R., Marra, M.  
Citation: Genome Res. 6 (9): 807-828 1996

**MAP DATA**

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PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Bc

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1: Genome Res 1996 Sep;6(9):807-28

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**Generation and analysis of 280,000 human expressed sequence tags.****Hillier LD, Lennon G, Becker M, Bonaldo MF, Chiapelli B, Chisoe S, Dietrich N, DuBuque T, Favello A, Gish W, Hawkins M, Hultman M, Kucaba T, Lacy M, Le M, Le N, Mardis E, Moore B, Morris M, Parsons Prange C, Rifkin L, Rohlfing T, Schellenberg K, Marra M, et al.**Genome Sequencing Center, Washington University School of Medicine, St. Louis, Missouri 63108, USA. [lhillier@watson.wustl.edu](mailto:lhillier@watson.wustl.edu)

We report the generation of 319,311 single-pass sequencing reactions (known expressed sequence tags, or ESTs) obtained from the 5' and 3' ends of 194,03 human cDNA clones. Our goal has been to obtain tag sequences from many different genes and to deposit these in the publicly accessible Data Base for Expressed Sequence Tags. Highly efficient automatic screening of the data allows deposition of the annotated sequences without delay. Sequences have been generated from 26 oligo(dT) primed directionally cloned libraries, of which 18 were normalized. The libraries were constructed using mRNA isolated from 17 different tissues representing three developmental states. Comparison of a subset of our data with nonredundant human mRNA and protein data bases show that the ESTs represent many known sequences and contain many that are novel. Analysis of protein families using Hidden Markov Models confirms this observation and supports the contention that although normalization reduces significantly the relative abundance of redundant cDNA clones, it does not result in the complete removal of members of gene families.

PMID: 8889549 [PubMed - indexed for MEDLINE]

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